Paper No. 28

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Ex parte STEPHEN H. HERRMANN,
ZHIJIAN LU, JOHN M. McCOY,
STEPHEN L. SWANBERG,
BRUCE WALKER, and OTTO YANG

Appeal No. 2002-1630
Application No. 09/175,713

ON BRIEF

Before WINTERS, ADAMS, and GRIMES, Administrative Patent Judges.

GRIMES, Administrative Patent Judge.

DECISION ON APPEAL

This is a decision on appeal under 35 U.S.C. § 134 from the examiner's final rejection of claims 1-14, 17, and 18, all of the claims remaining. Claims 5 and 6 are representative and read as follows:

5. A composition comprising an isolated polynucleotide encoding an amino-terminal-modified chemokine, wherein the amino-terminal-modified chemokine comprises at least one methionine, at least one aminooxypentane residue, or at least one GroHEK peptide covalently attached to the amino terminus of the chemokine, and wherein the amino-terminal-modified chemokine is derived from a chemokine selected from the group consisting of SDF-1α, SDF-1β, IP-10, Mig, GROα, GROβ, GROγ, interleukin-8, PF4, ENA-78, GCP-2, PBP,

CTAP-III, β-thromboglobulin, NAP-2, C10, DC-CK1, CKα1, CKα2, MCP-1, MCP-2, MCP-3, MCP-4, MIP-1α, MIP-1β, lymphotactin, ATAC, eotaxin, eotaxin-2, I-309, HCC-1, HCC-2, HCC-3, LARC/MIP-3α, MIP-3β, PARC, TARC, 6Ckine, ELC, SLC, CKβ4, CKβ6, CKβ7, CKβ8, CKβ9, CKβ11, CKβ12, CKβ13, and CX3C.

6. The composition of claim 1 wherein the polynucleotide is selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO: 6;

(b) a polynucleotide comprising the nucleotide sequence of the protein-coding sequence of the polynucleotide encoding met-hDSF[sic]-1α deposited under accession number ATCC 98506;

(c) a polynucleotide encoding an amino-terminal-modified chemokine comprising the amino acid sequence of SEQ ID NO:10;

(d) a polynucleotide encoding a protein comprising an amino-terminal fragment of the amino acid sequence of SEQ ID NO: 10;

(e) a polynucleotide comprising a nucleotide sequence complementary to any one of the polynucleotides specified in (a)-(d) above; and

(f) a polynucleotide capable of hybridizing at either (i) 4xSSC at 65°C or (ii) 50% formamide and 4XSSC at 42°C, to any one of the polynucleotides specified in (a)-(e) above.

The examiner relies on the following reference:

Proudfoot et al. (Proudfoot), "Extension of Recombinant Human RANTES by the Retention of the Initiating Methionine Produces a Potent Antagonist," Journal of Biological Chemistry, Vol. 271, No. 5, pp. 2599-2603 (1996)

Claims 1-14, 17, and 18 stand rejected under 35 U.S.C. § 112, first paragraph, as nonenabled.

Claims 1-14, 17, and 18 stand rejected under 35 U.S.C. § 112, first paragraph, as lacking an adequate written description.

We reverse the written description rejection with respect to all the claims. We also reverse the nonenablement rejection with respect to claims 6-9 but affirm it with respect to claims 1-5, 10-14, 17, and 18.

Background

"Chemokines (or chemotactic cytokines) are a class of cytokine molecules capable of chemotactically attracting migratory cells, and are involved in cell recruitment and activation in inflammation." Specification, page 1. "Most chemokines can be divided into two subgroups, CXC (alpha chemokines) or CC (beta chemokines)," and can also be further grouped into families, based on their amino acid sequence. Id., page 2.

The specification discloses that chemokines that have been modified at their amino terminus can interact with chemokine receptors and can have properties different from those of the unmodified chemokine. See, e.g., pages 16-17. Among the specific amino-terminal modifications disclosed in the specification are:

- addition of a methionine residue (page 18, lines 22-24)
- addition of an aminooxypentane residue (page 18, line 24, to page 19, line 4); and
- addition of a "GroHEK" peptide (page 19, lines 9-15).[1]

The specification provides working examples showing construction of polynucleotides encoding human stromal cell-derived factor 1α (hSDF-1α) and stromal cell-derived factor 1β (hSDF-1β), having either a methionine or a

[1] The GroHEK peptide is a 21-amino acid peptide, shown in SEQ ID NO:5. Specification, page 19, line 10.

GroHEK peptide attached to the amino terminus. See pages 42-45. The specification discloses that met-hSDF-1β stimulates higher calcium flux in cells than does unmodified hSDF-1β (pages 45-46) and that met-hSDF-1β and unmodified hSDF-1β are equally effective in blocking binding of other compounds to the chemokine receptor (pages 47-48). Finally, the specification discloses that met-hSDF-1β down-modulates expression of the chemokine receptor more effectively than unmodified hSDF-1β, and that this property results in an "enhanced ability of met-hSDF-1β to inhibit HIV infection," since the chemokine receptor is a co-receptor for HIV binding. See pages 48-52.

Discussion

1. Claim construction

Claims 1-5, 10-14, 17, and 18 stand or fall together, as do claims 6-9. Appeal Brief, page 4. We will consider claims 5 and 6 as representative.

Claim 5 is directed to a composition comprising a polynucleotide encoding an amino-terminal modified chemokine. The modified chemokine "comprises at least one methionine, at least one aminooxypentane residue, or at least one GroHEK peptide covalently attached to the amino terminus of the chemokine," and is "derived from" one of forty-nine enumerated chemokines. The specification states (page 17) that

> [a]n amino-terminal-modified chemokine is "derived from a chemokine" when the chemokine that has been modified at its amino terminus has itself been derived from a chemokine by any kind of alteration, addition, insertion, deletion, mutation, substitution, replacement, or other modification.

Thus, claim 5 encompasses an amino-terminal-modified chemokine "[that] has itself been derived from a chemokine by any kind of alteration, addition, insertion, deletion, mutation, substitution, replacement, or other modification." Therefore, we agree with the examiner's interpretation of claim 5: the claim encompasses "not only specified chemokines but also species comprising additions, insertions, deletions, mutations, substitutions, and replacements, as well as amino-terminal additions of varying lengths and compositions. . . . [Claim 5] encompass[es] all possible alterations to the known chemokine sequences." Examiner's Answer, page 4.

Claim 6, however, is not as broad. Claim 6 is limited to polynucleotides comprising SEQ ID NO:6 or a related polynucleotide (that is, polynucleotides encoding the same amino acid sequence, encoding an amino-terminal fragment thereof, complementary polynucleotides, or polynucleotides that hybridize under stringent conditions). Thus, claim 6 is limited to polynucleotides having a significant amount of structural similarity to a specified nucleotide sequence.

2. Written description

The examiner rejected the claims as not adequately described in the specification. According to the examiner, the claims encompass a very broad "genus" of chemokines, including the forty-nine enumerated proteins modified in one of three specified ways, but also including "species comprising additions, insertions, deletions, mutations, substitutions, and replacements, as well as amino-terminal additions." Examiner's Answer, page 4. The examiner

characterized the number of chemokines encompassed by the claims as "potentially infinite." Id.

In contrast, according to the examiner, the specification discloses the structure of only four species within the genus, and discloses the functional characteristics of only one. The examiner concluded that "[t]he disclosure of four closely related molecules, each a modified form of SDF-1 alpha or beta, and the functional characteristics of only one, are insufficient to describe the genus." Id.

Appellants argue that

> [t]he chemokines [recited in the claims] . . . were well known in the art by their common laboratory names long before the filing date of the instant application. . . . Therefore, coupled with information known in the art, Appellants have described a procedure of generating chemokine compositions modified at the amino-terminus and those of ordinary skill in the art would readily recognize that Appellants were in possession of the invention as claimed, i.e., a specifically enumerated list of chemokines having known sequences that are modified with GroHEK, methionine, or aminooxypentane at the amino-terminus.

Appeal Brief, pages 9-10.

The examiner "'bears the initial burden . . . of presenting a prima facie case of unpatentability.' . . . Insofar as the written description requirement is concerned, that burden is discharged by 'presenting evidence or reasons why persons skilled in the art would not recognize in the disclosure a description of the invention defined by the claims.'" In re Alton, 76 F.3d 1168, 1175, 37 USPQ2d 1578, 1583 (Fed. Cir. 1996). "[T]he written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics . . . i.e., complete or partial structure,

other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.'" Enzo Biochem, Inc. v. Gen-Probe Inc., 296 F.3d 1316, 1324, 63 USPQ2d 1609, 1613 (Fed. Cir. 2002) (emphasis omitted, bracketed material in original).

The Enzo court cited with approval the USPTO's Written Description Examination Guidelines See id. at 1327, 63 USPQ2d at 1615. Particularly relevant here, the court noted that the Written Description Guidelines include an example of "genus claims to nucleic acids based on their hybridization properties." Id. According to the Guidelines, "such claims may be adequately described if they hybridize under highly stringent conditions to known sequences because such conditions dictate that all species within the genus will be structurally similar." Id. The court directed the district court to consider the Guidelines in determining whether the claims at issue were adequately described. See id.

In this case, claims 6-9 are very similar to the genus claims defined by hybridization properties addressed in Enzo, in that the broadest category of nucleic acids defined by these claims are those that hybridize under stringent conditions to a structurally defined polynucleotide. To be consistent with Enzo, therefore, we consider how claims 6-9 would be treated under the Guidelines.

The Enzo court directed the district court to consider specifically Example 9 of the Written Description Guidelines.[2] See 296 F.3d at 1327, 63 USPQ2d at

[2] Example 9 of the Written Description Training Materials is available online at the USPTO web site (www.uspto.gov/web/offices/pac/writtendesc.pdf). See pages 35-37.

1615. That example describes a hypothetical application that discloses a single cDNA (SEQ ID NO:1) encoding a receptor-binding protein and claims nucleic acids that hybridize under "highly stringent conditions" to the complement of SEQ ID NO:1. On these facts, the Example concludes that the claimed genus of nucleic acids is adequately described, because "a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent hybridization conditions set forth in the claim yield structurally similar DNAs."

In our view, claims 6-9 would also be considered to have an adequate written description under the Guidelines. Claims 6-9 differ, in relevant part, from Example 9 of the Guidelines in that the hybridization conditions recited are only stringent rather than highly stringent. That is, the claims recite hybridization conditions of, e.g., 4xSSC and 65°C, while the Example recites conditions of 6xSSC and 65°C. Therefore, claims 6-9 allow the claimed polynucleotides to differ somewhat more in structure from the recited sequence. However, those skilled in the art would expect polynucleotides that hybridize under either stringent or highly stringent conditions to be similar in sequence (i.e., structure) to the target polynucleotide. In addition, the examiner has not adequately explained why the hybridizing polynucleotides of claims 6-9 are not adequately described in the specification.

Claims 1-5, 10-14, 17, and 18 present a closer question. As noted above, these claims are not limited to polynucleotides encoding chemokines that have been modified at their amino terminus; claim 5, for example, also encompasses

an amino-terminal-modified chemokine that "has itself been derived from a chemokine by any kind of alteration, addition, insertion, deletion, mutation, substitution, replacement, or other modification." Thus, we do not agree with Appellants' position (Appeal Brief, page 10) that the claims are limited to chemokines having known sequences, modified at the amino-terminus.

We do, however, agree with Appellants that the examiner has not shown claims 1-5, 10-14, 17, and 18 to be inadequately described. Again, Enzo provides the applicable standard. The Enzo court held that an adequate description could be provided by disclosing, for example, "complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." 296 F.3d at 1324, 63 USPQ2d at 1613.

Here, the claims encompass both known chemokines and chemokines that are "derived from" the known chemokines, modified at the amino terminus. This claim scope, however, does not render the specification's description inadequate. The claim limitation requiring that the claimed DNA encode a "chemokine" requires that the encoded protein have chemotactic activity. See the specification, page 17. Thus, even if the modified chemokine is derived from another chemokine, the modified chemokine must still possess the activity of the wild-type protein. As the examiner herself pointed out, changes in amino acid sequence have unpredictable effects on protein function. See the Examiner's Answer, page 6. Thus, those skilled in the art would reasonably expect that

chemokines that are "derived from" known chemokines would usually have to share a high degree of sequence similarity to the wild-type chemokine in order to also share its chemotactic activity.

This similarity of structure would appear to provide "complete or partial structure, other physical and/or chemical properties, [or] functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics," sufficient to describe the claimed compounds. Cf. Enzo, 296 F.3d at 1324, 63 USPQ2d at 1613.

For the above reasons, we reverse the examiner's rejection of claims 1-14, 17, and 18, for inadequate written description.

3. Enablement

The examiner also rejected all of the claims as non-enabled, although she acknowledged that the specification was enabling for the exemplified species met-SDF-1β. Examiner's Answer, page 6. The examiner also conceded that "generation of modified proteins is standard in the art," id., so that "one of skill in the art would be able [sic, would have been able] to make the claimed molecules." Id., page 7.

The examiner nonetheless concluded that the claims were not enabled throughout their full scope, based on several factors. First, the examiner found that the claims are extremely broad, in that they encompass modified chemokines that have no structural relationship to each other, as well as "a potentially infinite number of variants of these modified chemokines." See the Examiner's Answer, page 6. The examiner also found that the specification

provides only one working example of a modified chemokine having enhanced function relative to the unmodified chemokine, and the specification does not provide guidance to allow those of skill in the art to predictably identify and use other functional, amino-modified chemokines. Id., pages 6 and 7. Finally, the examiner found that the effect of additions or variations, within the naturally occurring amino acid sequence of a chemokine, have unpredictable effects on the function of the chemokine. Id., page 6.

The examiner therefore concluded that practicing the claimed invention throughout its full scope would have required undue experimentation. Id., page 7.

Appellants argue that the examiner has conceded that the specification would have enabled those skilled in the art to make the claimed products. Appeal Brief, page 12. With respect to the "how to use" prong of enablement, Appellants argue that

> [t]he test of enablement is whether one reasonably skilled in the art could make and use the invention from the disclosures in the application coupled with information known in the art without undue experimentation. The enablement requirement does not require that the disclosure provide any type of prediction with respect to the end results obtained from practicing the invention, which is what Examiner indicates is missing from the disclosure. In the instant case, Appellants have provided a detailed road map to enable one of ordinary skill in the art to practice the invention without undue experimentation. Appellants therefore submit that the "use" aspect of the claimed invention has also been met.

Appeal Brief, pages 12-13.

With respect to claims 6-9, Appellants argue that "[t]he narrow subset of modified chemokines in claims 6-9 are defined by SEQ ID NOs and ATCC

accession numbers that are disclosed in the specification and therefore enable one of ordinary skill in the art to practice the invention claimed." Appeal Brief, page 13.

The examiner bears the initial burden of showing that a claimed invention is not enabled. See In re Wright, 999 F.2d 1557, 1561-62, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993). "Although the statute does not say so, enablement requires that the specification teach those in the art to make and use the invention without 'undue experimentation.' . . . That some experimentation may be required is not fatal; the issue is whether the amount of experimentation required is 'undue.'" In re Vaeck, 947 F.2d 488, 495, 20 USPQ2d 1438, 1444 (Fed. Cir. 1991) (emphasis in original).

"Whether undue experimentation is needed is not a single, simple factual determination, but rather is a conclusion reached by weighing many factual considerations." In re Wands, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). Those considerations include the quantity of experimentation needed, the amount of guidance provided, the presence of working examples, the nature of the invention, the state of the prior art, the skill of those in the art, the degree of unpredictability involved, and the breadth of the claims. See id.

In this case, we agree with the examiner that the broadest of the claims on appeal (claims 1-5, 10-14, 17, and 18) are not enabled throughout their full scope. However, we conclude that the examiner's reasoning does not suffice to show nonenablement of the group of narrower claims (claims 6-9) that Appellants separately argue.

a. Claims 1-5, 10-14, 17, and 18

Claims 1-5, 10-14, 17, and 18 stand or fall together. Appeal Brief, page 4. We will consider claim 5 as representative. As discussed above (pages 3-4), claim 5 encompasses chemokines modified at the amino terminus, where the chemokine is either one of forty-nine naturally occurring chemokines, or a chemokine "derived from" any of the forty-nine enumerated chemokines "by any kind of alteration, addition, insertion, deletion, mutation, substitution, replacement, or other modification." Specification, page 17. We agree with the examiner that undue experimentation would have been required to practice the full scope of claim 5.

Most of the Wands factors favor a conclusion of nonenablement. The scope of claim 5 is enormous: the claim encompasses not just the forty-nine enumerated chemokines, modified in one of three ways at the amino terminus, but also encompasses an amino-terminal modified chemokine that can be derived from any of the enumerated chemokines by any kind of alteration. Thus, the claim encompasses any conceivable mutant or variant of any of the recited forty-nine chemokines, modified at the amino terminus, provided the modified chemokine displays chemotactic activity (i.e., it is still a chemokine).

The evidence of record also supports the examiner's position that the effect of changing a chemokine's amino acid sequence is unpredictable. The examiner cited Proudfoot as evidence that the addition of a methionine residue at the amino terminus has opposite effects on different chemokines. That is, the specification shows that the addition of an amino-terminal methionine increases

the activity of the chemokine SDF-1β, while Proudfoot shows that the same modification to the chemokine RANTES produces an inactive antagonist. See the Examiner's Answer, pages 12-13.

In addition, as the examiner noted, the working examples are limited to SDF-1α and SDF-1β, modified at the amino terminus with either a methionine or a GroHEK peptide. See the specification, pages 42-52. No working examples are provided showing the effect of aminooxypentane modification, nor are examples provided for any of the forty-seven other chemokines recited in claim 5, nor are examples provided showing the effect of modifying the sequence of a naturally occurring chemokine. The specification provides no guidance regarding which direction experimentation should proceed in making and using amino-terminal-modified chemokines differing from the naturally occurring chemokine "by any kind of alteration, addition, insertion, deletion, mutation, substitution, replacement, or other modification."

The examiner has conceded that those of skill in the art could have made the chemokine variants encompassed by the claims, but in view of the breadth of claim 5, a great deal of experimentation would have been involved in determining which of the variants were active and which were not. While Appellants are correct in arguing that there is no per se rule requiring predictability in extrapolating beyond the exemplified embodiments, predictability or the lack thereof is one of the factors to be considered in the Wands analysis. See Atlas Powder Co. v. E.I. Du Pont De Nemours & Co., 750 F.2d 1569, 1576, 224 USPQ 409, 414 (Fed. Cir. 1984): "Even if some of the claimed combinations were

inoperative, the claims are not necessarily invalid. . . . Of course, if the number of inoperative combinations becomes significant, and in effect forces one of ordinary skill in the art to experiment unduly in order to practice the claimed invention, the claims might indeed be invalid."

In view of the sweeping breadth of claim 5, and the absence of any basis for predicting which chemokine variants will retain activity, a great deal of experimentation would have been required to distinguish between operative and inoperative embodiments. We agree with the examiner that the amount of experimentation required to practice the full scope of claim 5 would have been undue. We therefore affirm the rejection of claims 1-5, 10-14, 17, and 18 for nonenablement.

b. Claims 6-9

The examiner included claims 6-9 in the rejection for nonenablement. The examiner explained that these claims were included in the rejection because they "encompass sequences comprising fragments as well as sequences identified by homology. They thus encompass sequences that vary widely from what is disclosed, and the skilled artisan would not predictably be able to use such molecules as disclosed." Examiner's Answer, page 15.

We reverse the rejection as it is applied to claims 6-9. These claims are of much narrower scope than, for example, claim 5. Claim 6 is representative. It encompasses the specific polynucleotide sequence of SEQ ID NO:6 (also defined by reference to an ATCC accession number), polynucleotides encoding

the same amino acid sequence, and the complements of these polynucleotides. These parts of the claim do not seem to bother the examiner.

The examiner's basis for rejecting the claim as nonenabled is the other two types of polynucleotide encompassed by claim 6: "(d) a polynucleotide encoding a protein comprising an amino-terminal fragment of the amino acid sequence of SEQ ID NO:10; . . . [and] (f) a polynucleotide capable of hybridizing at either (i) 4xSSC at 65°C or (ii) 50% formamide and 4xSSC at 42°C, to any of the polynucleotides specified in (a)-(e) above." The examiner has not adequately explained why practicing these parts of claim 6 would have required undue experimentation.

With respect to fragments, the examiner has presented no explanation of why undue experimentation would have been required to distinguish between active and inactive amino-terminal fragments of a specified polypeptide sequence. With respect to "hybridizing" polynucleotides, such as those recited in part (f) of claim 6, the specification defines the recited conditions as being "stringent hybridization conditions." See page 22. Thus, the polynucleotides encompassed by claims 6-9 do not include the "potentially infinite number of variants," Examiner's Answer, page 6, that are encompassed by claim 5 and that result in a requirement of undue experimentation.

We agree with Appellants that the set of modified cytokines encompassed by claims 6-9 is narrower than those encompassed by claim 5. The examiner has not adequately explained why undue experimentation would have been

required to practice the smaller genus of chemokines recited in claims 6-9. We therefore reverse the rejection of claims 6-9 for nonenablement.

Other Issues

1. Aminooxypentane-modified chemokines

The broader claims are directed to a polynucleotide that can encode a chemokine modified by addition of an aminooxypentane residue. However, the specification discloses that an aminooxypentane residue is added to the N-terminus of protein by a series of chemical reactions: first, a serine or threonine residue is converted to an aldehyde; then the aldehyde is reacted with aminooxypentane to form the desired aminooxypentane-modified chemokine. Since the aminooxypentane residue is added post-translationally, it is unclear how an aminooxypentane-modified chemokine can be encoded by a polynucleotide. It would appear that the polynucleotide encoding an aminooxypentane-modified chemokine would be the same as the polynucleotide encoding the unmodified chemokine.

If the claims are subject to further prosecution, the examiner should consider whether those that recite polynucleotides encoding an aminooxypentane-modified chemokine are sufficiently definite to meet the requirements of 35 U.S.C. § 112, second paragraph. In addition, if a polynucleotide encoding an aminooxypentane-modified chemokine is, in fact, the same as a polynucleotide encoding an unmodified chemokine, the examiner should consider whether any of the claims are anticipated by prior art disclosing a chemokine-encoding polynucleotide.

2. Claims 17 and 18

Claims 17 and 18 read as follows:

17. A composition comprising an isolated polynucleotide encoding an amino-terminal-modified chemokine, wherein the chemokine binds the fusin/CXCR4 chemokine receptor

18. A composition comprising an isolated polynucleotide encoding an amino-terminal-modified chemokine, wherein the amino-terminal-modified chemokine is a more effective inhibitor of HIV infection than the corresponding unmodified chemokine.

Thus, claims 17 and 18 are directed to genera of polynucleotides, defined by function rather than structure. The Federal Circuit has held that a genus of polynucleotides can be described by describing a "representative number" of species within the genus or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus." University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). See also Enzo, 296 F.3d at 1324, 63 USPQ2d at 1613: a compound can be described by "complete or partial structure, other physical and/or chemical properties, [or] functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

Although we reversed the examiner's written description rejection (which included claims 17 and 18), our decision was based only on the examiner's rationale for rejecting the claims, which did not separately address claims 17 and 18. If claims 17 and 18 are subject to further examination, the examiner should

consider whether the specification's description of the claimed genera meet the standards set out in Lilly and Enzo.

Summary

We reverse the rejection for inadequate written description because the examiner has not adequately explained why those skilled in the art would not have recognized the specification's description as showing that Appellants were in possession of the invention now claimed. We also reverse the rejection of claims 6-9 for nonenablement, because the examiner has not explained why undue experimentation would have been required to make and use fragments of the recited amino-terminal-modified chemokines, or variants encoded by polynucleotides that hybridize under stringent conditions. However, we affirm the rejection of claims 1-5, 10-14, 17, and 18 for nonenablement, because claim 5 reads on amino-terminal-modified chemokines that vary from the recited chemokines in any way and to any degree, and the specification does not provide sufficient guidance to practice the very broad scope of this claim. Claims 1-4, 10-14, 17, and 18 fall with claim 5.

No time period for taking any subsequent action in connection with this appeal may be extended under 37 CFR § 1.136(a).

AFFIRMED IN PART

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